RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: **US/09/830,762**   TIME: 14:11:04

Input Set : **A:\SEQLIST.txt**
Output Set: **N:\CRF3\11142001\I830762.raw**

```
 3 <110> APPLICANT: Shipp, Margaret
 4         Aguiar, Ricardo
 5         Yakushijin, Yoshi
 7 <120> TITLE OF INVENTION: LYMPHOMA ASSOCIATED MOLECULES AND USES THEREFOR
 9 <130> FILE REFERENCE: DFN-031US
11 <140> CURRENT APPLICATION NUMBER: US 09/830,762
12 <141> CURRENT FILING DATE: 2001-04-27
15 <150> PRIOR APPLICATION NUMBER: PCT/US99/25439
16 <151> PRIOR FILING DATE: 1999-10-29
18 <150> PRIOR APPLICATION NUMBER: US 60/106,383
19 <151> PRIOR FILING DATE: 1998-10-29
21 <150> PRIOR APPLICATION NUMBER: US 60/106,448
22 <151> PRIOR FILING DATE: 1998-10-30
24 <160> NUMBER OF SEQ ID NOS: 6
26 <170> SOFTWARE: PatentIn Ver. 2.0
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 3243
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (229)..(2790)
37 <400> SEQUENCE: 1
38 gggcttcgtg ttcctgggtg ctgaccgtgc actccccgcc gcccgaggac ttagagctct 60
40 ggaagtagct ctccagcttc cttcgtactc gggggccgga cttgtacacc cgcacgagga 120
42 gcggggacgg cgggcgcaga agtgggccac catatctgga aactacagtc tatgctttga 180
44 agcgcaaaag ggaataaaca tttaaagact cccccgggga cctggagg atg gac ttt 237
45                                                         Met Asp Phe
46                                                          1
48 tcc atg gtg gcc gga gca gca gct tac aat gaa aaa tca ggt agg att  285
49 Ser Met Val Ala Gly Ala Ala Ala Tyr Asn Glu Lys Ser Gly Arg Ile
50         5               10              15
52 acc tcg ctc tca ctc ttg ttt cag aaa gtc ttt gct cag atc ttt cct  333
53 Thr Ser Leu Ser Leu Leu Phe Gln Lys Val Phe Ala Gln Ile Phe Pro
54  20              25              30              35
56 cag tgg aga aag ggg aat aca gaa gaa tgt ctc ccc tac aag tgc tca  381
57 Gln Trp Arg Lys Gly Asn Thr Glu Glu Cys Leu Pro Tyr Lys Cys Ser
58              40              45              50
60 gag act ggt gct ctt gga gaa aac tat agt tgg caa att ccc att aac  429
61 Glu Thr Gly Ala Leu Gly Glu Asn Tyr Ser Trp Gln Ile Pro Ile Asn
62              55              60              65
64 cac aat gac ttc aaa att tta aaa aat aat gag cgt cag ctg tgt gaa  477
65 His Asn Asp Phe Lys Ile Leu Lys Asn Asn Glu Arg Gln Leu Cys Glu
66,          70              75              80
68 gtc ctc cag aat aag ttt ggc tgt atc tct acc ctg gtc tct cca gtt  525
69 Val Leu Gln Asn Lys Phe Gly Cys Ile Ser Thr Leu Val Ser Pro Val
70      85              90              95
```

ENTERED

```
 72 cag gaa ggc aac agc aaa tct ctg caa gtg ttc aga aaa atg ctg act    573
 73 Gln Glu Gly Asn Ser Lys Ser Leu Gln Val Phe Arg Lys Met Leu Thr
 74 100             105             110             115
 76 cct agg ata gag tta tca gtc tgg aaa gat gac ctc acc aca cat gct    621
 77 Pro Arg Ile Glu Leu Ser Val Trp Lys Asp Asp Leu Thr Thr His Ala
 78             120             125             130
 80 gtt gat gct gtg gtg aat gca gcc aat gaa gat ctt ctg cat ggg gga    669
 81 Val Asp Ala Val Val Asn Ala Ala Asn Glu Asp Leu Leu His Gly Gly
 82             135             140             145
 84 ggc ctg gcc ctg gcc ctg gta aaa gct ggt gga ttt gaa atc caa gaa    717
 85 Gly Leu Ala Leu Ala Leu Val Lys Ala Gly Gly Phe Glu Ile Gln Glu
 86         150             155             160
 88 gag agc aaa cag ttt gtt gcc aga tat ggt aaa gtg tca gct ggt gag    765
 89 Glu Ser Lys Gln Phe Val Ala Arg Tyr Gly Lys Val Ser Ala Gly Glu
 90     165             170             175
 92 ata gct gtc acg gga gca ggg agg ctt ccc tgc aaa cag atc atc cat    813
 93 Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln Ile Ile His
 94 180             185             190             195
 96 gct gtt ggg cct cgg tgg atg gaa tgg gat aaa cag gga tgt act gga    861
 97 Ala Val Gly Pro Arg Trp Met Glu Trp Asp Lys Gln Gly Cys Thr Gly
 98             200             205             210
100 aag ctg cag agg gcc att gta agt att ctg aat tat gtc atc tat aaa    909
101 Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val Ile Tyr Lys
102             215             220             225
104 aat act cac att aag aca gta gca att cca gcc ttg agc tct ggg att    957
105 Asn Thr His Ile Lys Thr Val Ala Ile Pro Ala Leu Ser Ser Gly Ile
106             230             235             240
108 ttt cag ttc cct ctg aat ttg tgt aca aag act att gta gag act atc   1005
109 Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val Glu Thr Ile
110     245             250             255
112 cgg gtt agt ttg caa ggg aag cca atg atg agt aat ttg aaa gaa att   1053
113 Arg Val Ser Leu Gln Gly Lys Pro Met Met Ser Asn Leu Lys Glu Ile
114 260             265             270             275
116 cac ctg gtg agc aat gag gac cct act gtt gct gcc ttt aaa gct gct   1101
117 His Leu Val Ser Asn Glu Asp Pro Thr Val Ala Ala Phe Lys Ala Ala
118             280             285             290
120 tca gaa ttc atc cta ggg aag agt gag ctg gga caa gaa acc acc cct   1149
121 Ser Glu Phe Ile Leu Gly Lys Ser Glu Leu Gly Gln Glu Thr Thr Pro
122     295             300             305
124 tct ttc aat gca atg gtc gtg aac aac ctg acc ctc cag att gtc cag   1197
125 Ser Phe Asn Ala Met Val Val Asn Asn Leu Thr Leu Gln Ile Val Gln
126         310             315             320
128 ggc cac att gaa tgg cag acg gca gat gta att gtt aat tct gta aac   1245
129 Gly His Ile Glu Trp Gln Thr Ala Asp Val Ile Val Asn Ser Val Asn
130     325             330             335
132 cca cat gat att aca gtt gga cct gtg gca aag tca att cta caa caa   1293
133 Pro His Asp Ile Thr Val Gly Pro Val Ala Lys Ser Ile Leu Gln Gln
134 340             345             350             355
136 gca gga gtt gaa atg aaa tcg gaa ttt ctt gcc aca aag gct aaa cag   1341
```

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/830,762   TIME: 14:11:04

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF3\11142001\I830762.raw

```
137 Ala Gly Val Glu Met Lys Ser Glu Phe Leu Ala Thr Lys Ala Lys Gln
138             360             365             370
140 ttt caa cgg tcc cag ttg gta ctg gtc aca aaa gga ttt aac ttg ttc   1389
141 Phe Gln Arg Ser Gln Leu Val Leu Val Thr Lys Gly Phe Asn Leu Phe
142             375             380             385
144 tgt aaa tat ata tac cat gta ctg tgg cat tca gaa ttt cct aaa cct   1437
145 Cys Lys Tyr Ile Tyr His Val Leu Trp His Ser Glu Phe Pro Lys Pro
146             390             395             400
148 cag ata tta aaa cat gca atg aag gag tgt ttg gaa aaa tgc att gag   1485
149 Gln Ile Leu Lys His Ala Met Lys Glu Cys Leu Glu Lys Cys Ile Glu
150     405             410             415
152 caa aat ata act tcc att tcc ttt cct gcc ctt ggg act gga aac atg   1533
153 Gln Asn Ile Thr Ser Ile Ser Phe Pro Ala Leu Gly Thr Gly Asn Met
154 420             425             430             435
156 gaa ata aag aag gaa aca gca gca gag att ttg ttt gat gaa gtt tta   1581
157 Glu Ile Lys Lys Glu Thr Ala Ala Glu Ile Leu Phe Asp Glu Val Leu
158             440             445             450
160 aca ttt gcc aaa gac cat gta aaa cac cag tta act gta aaa ttt gtg   1629
161 Thr Phe Ala Lys Asp His Val Lys His Gln Leu Thr Val Lys Phe Val
162             455             460             465
164 atc ttt cca aca gat ttg gag ata tat aag gct ttc agt tct gaa atg   1677
165 Ile Phe Pro Thr Asp Leu Glu Ile Tyr Lys Ala Phe Ser Ser Glu Met
166             470             475             480
168 gca aag agg tcc aag atg ctg agt ttg aac aat tac agt gtc ccc cag   1725
169 Ala Lys Arg Ser Lys Met Leu Ser Leu Asn Asn Tyr Ser Val Pro Gln
170     485             490             495
172 tca acc aga gag gag aaa aga gaa aat ggg ctt gaa gct aga tct cct   1773
173 Ser Thr Arg Glu Glu Lys Arg Glu Asn Gly Leu Glu Ala Arg Ser Pro
174 500             505             510             515
176 gcc atc aat ctg atg gga ttc aac gtg gaa gag atg tat gag gcc cac   1821
177 Ala Ile Asn Leu Met Gly Phe Asn Val Glu Glu Met Tyr Glu Ala His
178             520             525             530
180 gca tgg atc caa aga atc ctg agt ctc cag aac cac cac atc att gag   1869
181 Ala Trp Ile Gln Arg Ile Leu Ser Leu Gln Asn His His Ile Ile Glu
182             535             540             545
184 aat aat cat att ctg tac ctt ggg aga aag gaa cat gac att ttg tct   1917
185 Asn Asn His Ile Leu Tyr Leu Gly Arg Lys Glu His Asp Ile Leu Ser
186             550             555             560
188 cag ctt cag aaa act tca agt gtc tcc atc aca gaa att atc agc cca   1965
189 Gln Leu Gln Lys Thr Ser Ser Val Ser Ile Thr Glu Ile Ile Ser Pro
190     565             570             575
192 gga agg aca gag tta gag att gaa gga gcc cgg gct gac ctc att gag   2013
193 Gly Arg Thr Glu Leu Glu Ile Glu Gly Ala Arg Ala Asp Leu Ile Glu
194 580             585             590             595
196 gtg gtt atg aac att gaa gat atg ctt tgt aaa gta cag gag gaa atg   2061
197 Val Val Met Asn Ile Glu Asp Met Leu Cys Lys Val Gln Glu Glu Met
198             600             605             610
200 gca agg aaa aag gag cga ggc ctt tgg cgc tcg tta gga cag tgg act   2109
201 Ala Arg Lys Lys Glu Arg Gly Leu Trp Arg Ser Leu Gly Gln Trp Thr
```

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/830,762   TIME: 14:11:04

Input Set : A:\SEQLIST.txt
Output Set: N:\CRF3\11142001\I830762.raw

```
202          615                620                625
204 att cag caa caa aaa acc caa gac gaa atg aaa gaa aat atc ata ttt  2157
205 Ile Gln Gln Gln Lys Thr Gln Asp Glu Met Lys Glu Asn Ile Ile Phe
206          630                635                640
208 ctg aaa tgt cct gtg cct cca act caa gag ctt cta gat caa aag aaa  2205
209 Leu Lys Cys Pro Val Pro Pro Thr Gln Glu Leu Leu Asp Gln Lys Lys
210     645                650                655
212 cag ttt gaa aaa tgt ggt ttg cag gtt cta aag gtg gag aag ata gac  2253
213 Gln Phe Glu Lys Cys Gly Leu Gln Val Leu Lys Val Glu Lys Ile Asp
214 660                665                670                675
216 aat gag gtc ctt atg gct gcc ttt caa aga aag aag aaa atg atg gaa  2301
217 Asn Glu Val Leu Met Ala Ala Phe Gln Arg Lys Lys Lys Met Met Glu
218                680                685                690
220 gaa aaa ctg cac agg caa cct gtg agc cat agg ctg ttt cag caa gtc  2349
221 Glu Lys Leu His Arg Gln Pro Val Ser His Arg Leu Phe Gln Gln Val
222          695                700                705
224 cca tac cag ttc tgc aat gtg gta tgc aga gtt ggc ttt caa aga atg  2397
225 Pro Tyr Gln Phe Cys Asn Val Val Cys Arg Val Gly Phe Gln Arg Met
226          710                715                720
228 tac tcg aca cct tgc gat cca aaa tac gga gct ggc ata tac ttc acc  2445
229 Tyr Ser Thr Pro Cys Asp Pro Lys Tyr Gly Ala Gly Ile Tyr Phe Thr
230     725                730                735
232 aag aac ctc aaa aac ctg gca gag aag gcc aag aaa atc tct gct gca  2493
233 Lys Asn Leu Lys Asn Leu Ala Glu Lys Ala Lys Lys Ile Ser Ala Ala
234 740                745                750                755
236 gat aag ctg atc tat gtg ttt gag gct gaa gta ctc aca ggc ttc ttc  2541
237 Asp Lys Leu Ile Tyr Val Phe Glu Ala Glu Val Leu Thr Gly Phe Phe
238                760                765                770
240 tgc cag gga cat ccg tta aat att gtt ccc cca cca ctg agt cct gga  2589
241 Cys Gln Gly His Pro Leu Asn Ile Val Pro Pro Pro Leu Ser Pro Gly
242          775                780                785
244 gct ata gat ggt cat gac agt gtg gtt gac aat gtc tcc agc cct gaa  2637
245 Ala Ile Asp Gly His Asp Ser Val Val Asp Asn Val Ser Ser Pro Glu
246     790                795                800
248 acc ttt gtt att ttt agt ggc atg cag gct ata cct cag tat ttg tgg  2685
249 Thr Phe Val Ile Phe Ser Gly Met Gln Ala Ile Pro Gln Tyr Leu Trp
250     805                810                815
252 aca tgc acc cag gaa tat gta cag tca caa gat tac tca tca gga cca  2733
253 Thr Cys Thr Gln Glu Tyr Val Gln Ser Gln Asp Tyr Ser Ser Gly Pro
254 820                825                830                835
256 atg aga ccc ttt gca cag cat cct tgg agg gga ttc gca agt ggc agc  2781
257 Met Arg Pro Phe Ala Gln His Pro Trp Arg Gly Phe Ala Ser Gly Ser
258                840                845                850
260 cct gtt gat taatctctac atcattttaa cagctggtat ggccttacct       2830
261 Pro Val Asp
263 tgggtgaact aaccaaataa tgaccatcga tggctcaaag agtggcttga atatatccca 2890
265 tgggttatct gtatggactg actgggttat tgaaaggact agccacatac tagcatctta 2950
267 gtgcctttat ctgtctttat gtcttggggt tggggtaggt agataccaaa tgaaacactt 3010
269 tcaggacctt ccttcctctt gcagttgttc tttaatctcc tttactagag gagataaata 3070
```

```
271 ttttgcatat aatgaagaaa tttttctagt atataacgca ggcctttat tttctaaaat 3130
273 gatgatagta taaaaatgtt aggataacag aatgattta gattttccag agaatattat 3190
275 aaagtgcttt aggtatgaaa ataaatcatc tttgtctgat taaaaaaaaa aaa       3243
278 <210> SEQ ID NO: 2
279 <211> LENGTH: 854
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 2
284 Met Asp Phe Ser Met Val Ala Gly Ala Ala Ala Tyr Asn Glu Lys Ser
285 1               5                   10                  15
287 Gly Arg Ile Thr Ser Leu Ser Leu Leu Phe Gln Lys Val Phe Ala Gln
288             20                  25                  30
290 Ile Phe Pro Gln Trp Arg Lys Gly Asn Thr Glu Glu Cys Leu Pro Tyr
291         35                  40                  45
293 Lys Cys Ser Glu Thr Gly Ala Leu Gly Glu Asn Tyr Ser Trp Gln Ile
294     50                  55                  60
296 Pro Ile Asn His Asn Asp Phe Lys Ile Leu Lys Asn Asn Glu Arg Gln
297 65                  70                  75                  80
299 Leu Cys Glu Val Leu Gln Asn Lys Phe Gly Cys Ile Ser Thr Leu Val
300                 85                  90                  95
302 Ser Pro Val Gln Glu Gly Asn Ser Lys Ser Leu Gln Val Phe Arg Lys
303             100                 105                 110
305 Met Leu Thr Pro Arg Ile Glu Leu Ser Val Trp Lys Asp Asp Leu Thr
306             115                 120                 125
308 Thr His Ala Val Asp Ala Val Val Asn Ala Ala Asn Glu Asp Leu Leu
309     130                 135                 140
311 His Gly Gly Gly Leu Ala Leu Ala Leu Val Lys Ala Gly Gly Phe Glu
312 145                 150                 155                 160
314 Ile Gln Glu Glu Ser Lys Gln Phe Val Ala Arg Tyr Gly Lys Val Ser
315                 165                 170                 175
317 Ala Gly Glu Ile Ala Val Thr Gly Ala Gly Arg Leu Pro Cys Lys Gln
318             180                 185                 190
320 Ile Ile His Ala Val Gly Pro Arg Trp Met Glu Trp Asp Lys Gln Gly
321         195                 200                 205
323 Cys Thr Gly Lys Leu Gln Arg Ala Ile Val Ser Ile Leu Asn Tyr Val
324     210                 215                 220
326 Ile Tyr Lys Asn Thr His Ile Lys Thr Val Ala Ile Pro Ala Leu Ser
327 225                 230                 235                 240
329 Ser Gly Ile Phe Gln Phe Pro Leu Asn Leu Cys Thr Lys Thr Ile Val
330             245                 250                 255
332 Glu Thr Ile Arg Val Ser Leu Gln Gly Lys Pro Met Met Ser Asn Leu
333             260                 265                 270
335 Lys Glu Ile His Leu Val Ser Asn Glu Asp Pro Thr Val Ala Ala Phe
336         275                 280                 285
338 Lys Ala Ala Ser Glu Phe Ile Leu Gly Lys Ser Glu Leu Gly Gln Glu
339     290                 295                 300
341 Thr Thr Pro Ser Phe Asn Ala Met Val Val Asn Asn Leu Thr Leu Gln
342 305                 310                 315                 320
344 Ile Val Gln Gly His Ile Glu Trp Gln Thr Ala Asp Val Ile Val Asn
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/830,762**

DATE: 11/14/2001
TIME: 14:11:05

Input Set : **A:\SEQLIST.txt**
Output Set: **N:\CRF3\11142001\I830762.raw**

L:1241 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 6, CDS LOCATION:1..2478